44. A method according to claim 41, wherein, in the presence of a Mn^{2+} cofactor, said thermostable ligase has a 12 fold higher fidelity than wild-type *Thermus thermophilus* ligase, when sealing a ligation junction between a pair of oligonucleotide probes hybridized to a target sequence where there is a mismatch with the oligonucleotide probe having its 3' end abutting the ligation junction at the base immediately adjacent to the ligation junction.

45. A method according to claim 42, wherein the thermostable ligase has an arginine adjacent its active site lysine in the KXDG motif where X is any amino acid.

46. A method according to claim 41, wherein the thermostable ligase has a molecular weight of 78 to 81 kDa as determined by SDS-PAGE.

47. A method according to claim 41, wherein the thermostable ligase has an amino acid sequence of SEQ. ID. No. 1.

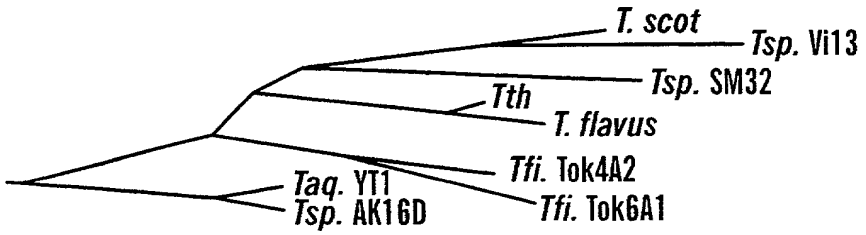

FIG. 1A

113	YTVERKVDGLSVNLYYE	129	.....	231	LEE	...	TG	239	..... 285 PFEADGVVVKLD 296 *Tsp.* AK16D
	YTVEHKVDGLSVNLYYE		.....		LEE	...	TG		..... PFEADGVVVKLD *Taq.* YT1
	YTVEHKVDGLSVNLYYE		.....		LEEVEREG				..... PFEADGVVVKLD *Tth*
	YTVEHKVDGLSVNLYYE		.....		LEEVEREG				..... PFEADGVVVKLD *T. flavus*
	YTVEHKVDGLSVNLYYE		.....		LEE	...	SG		..... PFEADGVVVKMD *Tfi.* Tok4A2
	YTVEHKVDGLSVNLYYE		.....		LEE	...	SG		..... PFEADGVVVKLD *Tfi.* Tok6A1
	YTVEHKVDGLSVNLYYE		.....		LEE	...	SG		..... PFEADGVVVKLD *Tsp.* SM32
	YTVEHKVDGLSVNLYYE		.....		LEE	...	SG		..... PFEADGVVVKLD *Tsp.* Vil3
	YTVEHKVDGLSVNLYYE		.....		LEE	...	SG		..... PFEADGVVVKLD *T. scot*

FIG. 1B

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MTLEEARRRVNELRDLIRYHNYLYYVLDAPEISDAEYDRLLRELKELEERFPELKSPDSP    60
TEQVGARPLEATFRPVRHPTRMYSLDNAFSLDEVRAFEERIERALGRKGPFLYTVERKVD   120
GLSVNLYYEEGILVFGATRGDGETGEEVTQNLLTIPTIPRRLTGVPDRLEVRGEVYMPIE   180
AFLRLNQELEEAGERIFKNPRNAAAGSLRQKDPRVTARRGLRATFYALGLGLEETGLKSQ   240
HDLLLWLRERGFPVEHGFTRALGAEGVEEVYQAWLKERRKLPFEADGVVVKLDDLALWRE   300
LGYTARTPRFALAYKFPAEEKETRLLSVAFQVGRTGRITPVGVLEPVFIEGSEVSRVTLH   360
NESFIEELDVRIGDWVLVHKAGGVIPEVLRVLKERRTGEEKPIIWPENCPECGHALIKEG   420
KVHRCPNPLCPAKRFEAIRHYASRKAMDIQGLGEKLIEKLLEKGLVRDVADLYRLKKEDL   480
VNLERMGEKSAENLLRQIEESKGRGLERLLYALGLPGVGEVLARNLALRFGHMDRLLEAG   540
LEDLLEVEGVGELTARAILNTLKDPEFRDLVRRLKEAGVEMEAKEREGEALKGLTFVITG   600
ELSRPREEVKALLRRLGAKVTDSVSRKTSFLVVGENPGSKLEKARALGVPTLSEEELYRL   660
IEERTGKDPRALTA                                                  674
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FIG. 1C

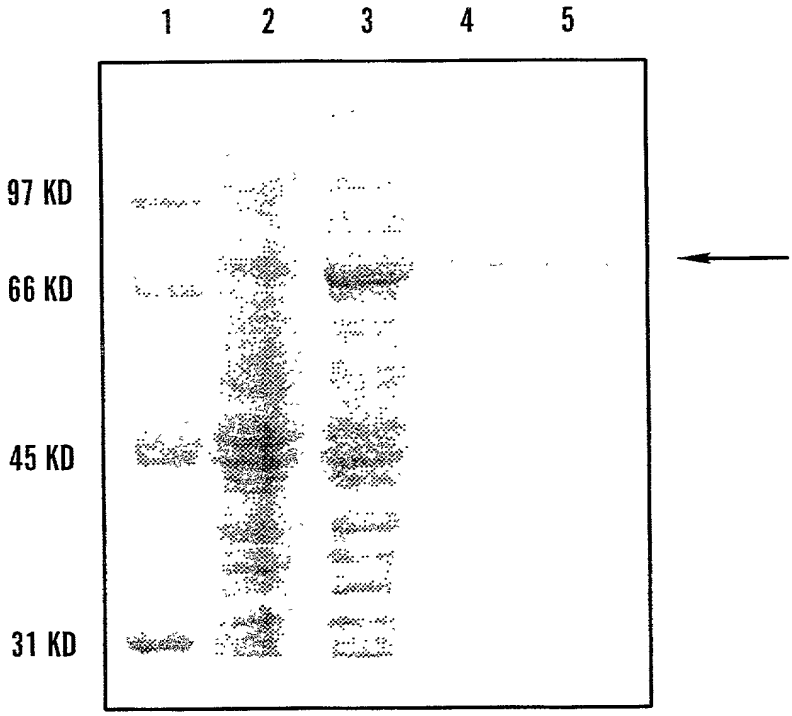

FIG. 2